

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
- (ii) TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Immunex Corporation, Law Department
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Power Macintosh
 - (C) OPERATING SYSTEM: Apple Operating System 7.5.5
 - (D) SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 22 DECEMBER 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: USSN 60/064,671
 - (B) FILING DATE: 14 OCTOBER 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: USSN 08/813,509
 - (B) FILING DATE: 07 MARCH 1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: USSN 08/772,330 (60/064,671)
 - (B) FILING DATE: 23 DECEMBER 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Perkins, Patricia Anne
 - (B) REGISTRATION NUMBER: 34,693
 - (C) REFERENCE/DOCKET NUMBER: 2852-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206)587-0430
 - (B) TELEFAX: (206)233-0644

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMO SAPIENS

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
(B) CLONE: 9D-8A

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 93..1868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTGCTGCTG CTCTGCGCGC TGCTCGCCCG GCTGCAGTTT TATCCAGAAA GAGCTGTGTG	60
GACTCTCTGC CTGACCTCAG TGTTCTTTTC AG GTG GCT TTG CAG ATC GCT CCT	113
Val Ala Leu Gln Ile Ala Pro	
1 5	
CCA TGT ACC AGT GAG AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC	161
Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn	
10 15 20	
AAA TGT GAA CCA GGA AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT	209
Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser	
25 30 35	
GAC AGT GTA TGT CTG CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG	257
Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp	
40 45 50 55	
AAT GAA GAA GAT AAA TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG	305
Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys	
60 65 70	
GCC CTG GTG GCC GTG GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC	353
Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys	
75 80 85	
GCG TGC ACG GCT GGG TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC	401
Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg	
90 95 100	
CGC AAC ACC GAG TGC GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG	449
Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln	
105 110 115	
CTC AAC AAG GAC ACA GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT	497
Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser	
120 125 130 135	
GAT GCC TTT TCC TCC ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC	545
Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr	
140 145 150	
TTC CTT GGA AAG AGA GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG	593
Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala	
155 160 165	
GTT TGC AGT TCT TCT CTG CCA GCT AGA AAA CCA CCA AAT GAA CCC CAT	641
Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His	
170 175 180	
GTT TAC TTG CCC GGT TTA ATA ATT CTG CTT CTC TTC GCG TCT GTG GCC	689
Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala	
185 190 195	

CTG Leu 200	GTG Val	GCT Ala	GCC Ala	ATC Ile	ATC Ile 205	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 210	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 215	737
GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 220	TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 225	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 230	CGC Arg	785
CTA Leu	AGT Ser	GGA Gly	GAT Asp 235	AAG Lys	GAG Glu	TCC Ser	TCA Ser	GGT Gly 240	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 245	ACA Thr	CAC His	833
ACG Thr	GCA Ala	AAC Asn 250	TTT Phe	GGT Gly	CAG Gln	CAG Gln	GGA Gly 255	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 260	TTA Leu	CTG Leu	CTG Leu	881
ACT Thr	CTG Leu 265	GAG Glu	GAG Glu	AAG Lys	ACA Thr	TTT Phe 270	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 275	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	929
GGT Gly 280	GGT Gly	GTC Val	TGT Cys	CAG Gln	GGC Gly 285	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 290	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 295	977
GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 300	ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 305	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 310	GAG Glu	1025
GAA Glu	GAC Asp	AGC Ser	TTC Phe 315	AGA Arg	CAG Gln	ATG Met	CCC Pro	ACA Thr 320	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG Met 325	GAC Asp	AGG Arg	1073
CCC Pro	TCC Ser	CAG Gln 330	CCC Pro	ACA Thr	GAC Asp	CAG Gln	TTA Leu 335	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG Glu 340	CCT Pro	GGA Gly	AGC Ser	1121
AAA Lys	TCC Ser 345	ACA Thr	CCT Pro	CCT Pro	TTC Phe	TCT Ser 350	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 355	GGG Gly	GAG Glu	AAT Asn	GAC Asp	1169
AGT Ser 360	TTA Leu	AGC Ser	CAG Gln	TGC Cys 365	TTC Phe	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 370	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu 375	1217
AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 380	GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 385	ACT Thr	GAT Asp	TGG Trp	ACT Thr 390	CCC Pro	ATG Met	1265
TCC Ser	TCT Ser	GAA Glu 395	AAC Asn	TAC Tyr	TTG Leu	CAA Gln	AAA Lys	GAG Glu 400	GTG Val	GAC Asp	AGT Ser	GGC Gly 405	CAT His	TGC Cys	CCG Pro	1313
CAC His	TGG Trp 410	GCA Ala	GCC Ala	AGC Ser	CCC Pro	AGC Ser	CCC Pro 415	AAC Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 420	TGC Cys	ACA Thr	GGC Gly	1361
TGC Cys	CGG Arg 425	AAC Asn	CCT Pro	CCT Pro	GGG Gly 430	GAG Glu	GAC Asp	TGT Cys	GAA Glu	CCC Pro 435	CTC Leu	GTG Val	GGT Gly	TCC Ser	CCA Pro	1409
AAA Lys 440	CGT Arg	GGA Gly	CCC Pro	TTG Leu	CCC Pro 445	CAG Gln	TGC Cys	GCC Ala	TAT Tyr	GGC Gly 450	ATG Met	GGC Gly	CTT Leu	CCC Pro	CCT Pro 455	1457
GAA Glu	GAA Glu	GAA Glu	GCC Ala	AGC Ser 460	AGG Arg	ACG Thr	GAG Glu	GCC Ala	AGA Arg 465	GAC Asp	CAG Gln	CCC Pro	GAG Glu	GAT Asp 470	GGG Gly	1505

GCT Ala	GAT Asp	GGG Gly	AGG Arg 475	CTC Leu	CCA Pro	AGC Ser	TCA Ser	GCG Ala 480	AGG Arg	GCA Ala	GGT Gly	GCC Ala	GGG Gly 485	TCT Ser	GGA Gly	1553		
AGC Ser	TCC Ser	CCT Pro 490	GGT Gly	GGC Gly	CAG Gln	TCC Ser	CCT Pro 495	GCA Ala	TCT Ser	GGA Gly	AAT Asn	GTG Val 500	ACT Thr	GGA Gly	AAC Asn	1601		
AGT Ser	AAC Asn 505	TCC Ser	ACG Thr	TTC Phe	ATC Ile	TCC Ser 510	AGC Ser	GGG Gly	CAG Gln	GTG Val	ATG Met 515	AAC Asn	TTC Phe	AAG Lys	GGC Gly	1649		
GAC Asp 520	ATC Ile	ATC Ile	GTG Val	GTC Val	TAC Tyr 525	GTC Val	AGC Ser	CAG Gln	ACC Thr	TCG Ser 530	CAG Gln	GAG Glu	GGC Gly	GCG Ala	GCG Ala 535	1697		
GCG Ala	GCT Ala	GCG Ala	GAG Glu	CCC Pro 540	ATG Met	GGC Gly	CGC Arg	CCG Pro	GTG Val 545	CAG Gln	GAG Glu	GAG Glu	ACC Thr	CTG Leu 550	GCG Ala	1745		
CGC Arg	CGA Arg	GAC Asp 555	TCC Ser	TTC Phe	GCG Ala	GGG Gly	AAC Asn	GGC Gly 560	CCG Pro	CGC Arg	TTC Phe	CCG Pro	GAC Asp 565	CCG Pro	TGC Cys	1793		
GGC Gly	GGC Gly	CCC Pro 570	GAG Glu	GGG Gly	CTG Leu	CGG Arg	GAG Glu 575	CCG Pro	GAG Glu	AAG Lys	GCC Ala	TCG Ser 580	AGG Arg	CCG Pro	GTG Val	1841		
CAG Gln 585	GAG Glu	CAA Gln	GGC Gly	GGG Gly	GCC Ala	AAG Lys 590	GCT Ala	TGA	GCGCCCCCA TGGCTGGGAG							1888		
CCCGAAGCTC			GGAGCCAGGG			CTCGCGAGGG			CAGCACCGCA			GCCTCTGCCC			CAGCCCCGGC			1948
CAGCCAGGGA			TCGATCGGTA			CAGTCGAGGA			AGACCACCCG			GCATTCTCTG			CCCACTTTGC			2008
CTTCCAGGAA			ATGGGCTTTT			CAGGAAGTGA			ATTGATGAGG			ACTGTCCCCA			TGCCACGGA			2068
TGCTCAGCAG			CCCGCCGCAC			TGGGGCAGAT			GTCTCCCCTG			CCACTCCTCA			AACTCGCAGC			2128
AGTAATTTGT			GGCACTATGA			CAGCTATTTT			TATGACTATC			CTGTTCTGTG			GGGGGGGGGT			2188
CTATGTTTTT			CCCCCATATT			TGTATTCCTT			TTCATAACTT			TTCTTGATAT			CTTTCCTCCC			2248
TCTTTTTTAA			TGTAAGGTT			TTCTCAAAA			TTCTCCTAAA			GGTGAGGGTC			TCTTCTTTTT			2308
CTCTTTTTCCT			TTTTTTTTTTC			TTTTTTTTTGGC			AACCTGGCTC			TGGCCCAGGC			TAGAGTGCAG			2368
TGGTGCGATT			ATAGCCCGGT			GCAGCCTCTA			ACTCCTGGGC			TCAAGCAATC			CAAGTGATCC			2428
TCCCACCTCA			ACCTTCGGAG			TAGCTGGGAT			CACAGCTGCA			GGCCACGCCC			AGCTTCCTCC			2488
CCCCGACTCC			CCCCCCCCCAG			AGACACGGTC			CCACCATGTT			ACCCAGCCTG			GTCTCAAACT			2548
CCCCAGCTAA			AGCAGTCCTC			CAGCCTCGGC			CTCCCAAAGT			ACTGGGATTA			CAGGCGTGAG			2608
CCCCCACGCT			GGCCTGCTTT			ACGTATTTTC			TTTTGTGCCC			CTGCTCACAG			TGTTTTAGAG			2668
ATGGCTTTCC			CAGTGTGTGT			TCATTGTAAA			CACTTTTGGG			AAAGGGCTAA			ACATGTGAGG			2728
CCTGGAGATA			GTTGCTAAGT			TGCTAGGAAC			ATGTGGTGGG			ACTTTCATAT			TCTGAAAAAT			2788
GTTCTATATT			CTCATTTTTT			TAAAAGAAAG			AAAAAAGGAA			ACCCGATTTA			TTTCTCCTGA			2848
ATCTTTTTTAA			GTTTGTGTGCG			TTCCTTAAGC			AGAACTAAGC			TCAGTATGTG			ACCTTACCCG			2908
CTAGGTGGTT			AATTTATCCA			TGCTGGCAGA			GGCACTCAGG			TACTTGGTAA			GCAAATTTCT			2968
AAAAC TCCAA			GTTGCTGCAG			CTTGGCATTC			TTCTTATTCT			AGAGGTCTCT			CTGGAAAAGA			3028

TGGAGAAAAT GAACAGGACA TGGGGCTCCT GGAAAGAAAG GGCCCGGGAA GTTCAAGGAA 3088
 GAATAAAGTT GAAATTTTAA AAAAAAA 3115

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys His Tyr Glu
 1 5 10 15
 His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys Tyr Met Ser
 20 25 30
 Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu Pro Cys Gly Pro
 35 40 45
 Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys Cys Leu Leu His
 50 55 60
 Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val Val Ala Gly Asn
 65 70 75 80
 Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly Tyr His Trp Ser
 85 90 95
 Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys Ala Pro Gly Leu
 100 105 110
 Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr Val Cys Lys Pro
 115 120 125
 Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser Thr Asp Lys Cys
 130 135 140
 Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg Val Glu His His
 145 150 155 160
 Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser Leu Pro Ala Arg
 165 170 175
 Lys Pro Pro Asn Glu Pro His Val Tyr Leu Pro Gly Leu Ile Ile Leu
 180 185 190
 Leu Leu Phe Ala Ser Val Ala Leu Val Ala Ala Ile Ile Phe Gly Val
 195 200 205
 Cys Tyr Arg Lys Lys Gly Lys Ala Leu Thr Ala Asn Leu Trp His Trp
 210 215 220
 Ile Asn Glu Ala Cys Gly Arg Leu Ser Gly Asp Lys Glu Ser Ser Gly
 225 230 235 240
 Asp Ser Cys Val Ser Thr His Thr Ala Asn Phe Gly Gln Gln Gly Ala
 245 250 255
 Cys Glu Gly Val Leu Leu Leu Thr Leu Glu Glu Lys Thr Phe Pro Glu
 260 265 270
 Asp Met Cys Tyr Pro Asp Gln Gly Gly Val Cys Gln Gly Thr Cys Val
 275 280 285

Gly Gly Gly Pro Tyr Ala Gln Gly Glu Asp Ala Arg Met Leu Ser Leu
 290 295 300
 Val Ser Lys Thr Glu Ile Glu Glu Asp Ser Phe Arg Gln Met Pro Thr
 305 310 315 320
 Glu Asp Glu Tyr Met Asp Arg Pro Ser Gln Pro Thr Asp Gln Leu Leu
 325 330 335
 Phe Leu Thr Glu Pro Gly Ser Lys Ser Thr Pro Pro Phe Ser Glu Pro
 340 345 350
 Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln Cys Phe Thr Gly Thr
 355 360 365
 Gln Ser Thr Val Gly Ser Glu Ser Cys Asn Cys Thr Glu Pro Leu Cys
 370 375 380
 Arg Thr Asp Trp Thr Pro Met Ser Ser Glu Asn Tyr Leu Gln Lys Glu
 385 390 395 400
 Val Asp Ser Gly His Cys Pro His Trp Ala Ala Ser Pro Ser Pro Asn
 405 410 415
 Trp Ala Asp Val Cys Thr Gly Cys Arg Asn Pro Pro Gly Glu Asp Cys
 420 425 430
 Glu Pro Leu Val Gly Ser Pro Lys Arg Gly Pro Leu Pro Gln Cys Ala
 435 440 445
 Tyr Gly Met Gly Leu Pro Pro Glu Glu Glu Ala Ser Arg Thr Glu Ala
 450 455 460
 Arg Asp Gln Pro Glu Asp Gly Ala Asp Gly Arg Leu Pro Ser Ser Ala
 465 470 475 480
 Arg Ala Gly Ala Gly Ser Gly Ser Ser Pro Gly Gly Gln Ser Pro Ala
 485 490 495
 Ser Gly Asn Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly
 500 505 510
 Gln Val Met Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln
 515 520 525
 Thr Ser Gln Glu Gly Ala Ala Ala Ala Glu Pro Met Gly Arg Pro
 530 535 540
 Val Gln Glu Glu Thr Leu Ala Arg Arg Asp Ser Phe Ala Gly Asn Gly
 545 550 555 560
 Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu Arg Glu Pro
 565 570 575
 Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala Lys Ala
 580 585 590

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
(B) CLONE: 9D-15C
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 39..1391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC	53
Met Ala Pro Arg Ala	
1 5	
CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC	101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu	
10 15 20	
GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG	149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu	
25 30 35	
AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA	197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly	
40 45 50	
AAG TAC ATG TCT TCT AAA TGC ACT ACT ACC TCT GAC AGT GTA TGT CTG	245
Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser Asp Ser Val Cys Leu	
55 60 65	
CCC TGT GGC CCG GAT GAA TAC TTG GAT AGC TGG AAT GAA GAA GAT AAA	293
Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp Asn Glu Glu Asp Lys	
70 75 80 85	
TGC TTG CTG CAT AAA GTT TGT GAT ACA GGC AAG GCC CTG GTG GCC GTG	341
Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys Ala Leu Val Ala Val	
90 95 100	
GTC GCC GGC AAC AGC ACG ACC CCC CGG CGC TGC GCG TGC ACG GCT GGG	389
Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys Ala Cys Thr Ala Gly	
105 110 115	
TAC CAC TGG AGC CAG GAC TGC GAG TGC TGC CGC CGC AAC ACC GAG TGC	437
Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg Arg Asn Thr Glu Cys	
120 125 130	
GCG CCG GGC CTG GGC GCC CAG CAC CCG TTG CAG CTC AAC AAG GAC ACA	485
Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln Leu Asn Lys Asp Thr	
135 140 145	
GTG TGC AAA CCT TGC CTT GCA GGC TAC TTC TCT GAT GCC TTT TCC TCC	533
Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser Asp Ala Phe Ser Ser	
150 155 160 165	
ACG GAC AAA TGC AGA CCC TGG ACC AAC TGT ACC TTC CTT GGA AAG AGA	581
Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr Phe Leu Gly Lys Arg	
170 175 180	
GTA GAA CAT CAT GGG ACA GAG AAA TCC GAT GCG GTT TGC AGT TCT TCT	629
Val Glu His His Gly Thr Glu Lys Ser Asp Ala Val Cys Ser Ser Ser	
185 190 195	

CTG Leu	CCA Pro	GCT Ala 200	AGA Arg	AAA Lys	CCA Pro	CCA Pro	AAT Asn 205	GAA Glu	CCC Pro	CAT His	GTT Val	TAC Tyr 210	TTG Leu	CCC Pro	GGT Gly	677
TTA Leu	ATA Ile 215	ATT Ile	CTG Leu	CTT Leu	CTC Leu	TTC Phe 220	GCG Ala	TCT Ser	GTG Val	GCC Ala	CTG Leu 225	GTG Val	GCT Ala	GCC Ala	ATC Ile	725
ATC Ile 230	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 235	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 240	GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 245	773
TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 250	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 255	CGC Arg	CTA Leu	AGT Ser	GGA Gly	GAT Asp 260	AAG Lys	821
GAG Glu	TCC Ser	TCA Ser	GGT Gly 265	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 270	ACA Thr	CAC His	ACG Thr	GCA Ala	AAC Asn 275	TTT Phe	GGT Gly	869
CAG Gln	CAG Gln	GGA Gly 280	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 285	TTA Leu	CTG Leu	CTG Leu	ACT Thr 290	CTG Leu	GAG Glu	GAG Glu	AAG Lys	917
ACA Thr 295	TTT Phe	CCA Pro	GAA Glu	GAT Asp	ATG Met 300	TGC Cys	TAC Tyr	CCA Pro	GAT Asp	CAA Gln 305	GGT Gly	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
GGC Gly 310	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 315	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 320	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 325	1013
ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 330	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 335	GAG Glu	GAA Glu	GAC Asp	AGC Ser	TTC Phe 340	AGA Arg	1061
CAG Gln	ATG Met	CCC Pro	ACA Thr 345	GAA Glu	GAT Asp	GAA Glu	TAC Tyr 350	ATG Met	GAC Asp	AGG Arg	CCC Pro	TCC Ser	CAG Gln 355	CCC Pro	ACA Thr	1109
GAC Asp	CAG Gln 360	TTA Leu	CTG Phe	TTC Leu	CTC Leu	ACT Thr 365	GAG Glu 365	CCT Pro	GGA Gly	AGC Ser	AAA Lys	TCC Ser 370	ACA Thr	CCT Pro	CCT Pro	1157
TTC Phe 375	TCT Ser	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 380	GGG Gly	GAG Glu	AAT Asn	GAC Asp 385	AGT Ser	TTA Leu	AGC Ser	CAG Gln	TGC Cys	1205
TTC Phe 390	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 395	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu 400	AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 405	1253
GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 410	ACT Thr	GAT Asp	TGG Trp	ACT Thr	CCC Pro 415	ATG Met	TCC Ser	TCT Ser	GAA Glu 420	AAC Asn	TAC Tyr	1301
TTG Leu	CAA Gln	AAA Lys 425	GAG Glu	GTG Val	GAC Asp	AGT Ser	GGC Gly	CAT His 430	TGC Cys	CCG Pro	CAC His	TGG Trp	GCA Ala 435	GCC Ala	AGC Ser	1349
CCC Pro	AGC Ser	CCC Pro	AAC Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 445	TGC Cys	ACA Thr	GGC Gly	TGC Cys	CGG Arg 450	AAC Asn			1391

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met  Ala  Pro  Arg  Ala  Arg  Arg  Arg  Arg  Pro  Leu  Phe  Ala  Leu  Leu  Leu
 1          5          10          15
Leu  Cys  Ala  Leu  Leu  Ala  Arg  Leu  Gln  Val  Ala  Leu  Gln  Ile  Ala  Pro
          20          25          30
Pro  Cys  Thr  Ser  Glu  Lys  His  Tyr  Glu  His  Leu  Gly  Arg  Cys  Cys  Asn
          35          40          45
Lys  Cys  Glu  Pro  Gly  Lys  Tyr  Met  Ser  Ser  Lys  Cys  Thr  Thr  Thr  Ser
          50          55          60
Asp  Ser  Val  Cys  Leu  Pro  Cys  Gly  Pro  Asp  Glu  Tyr  Leu  Asp  Ser  Trp
 65          70          75          80
Asn  Glu  Glu  Asp  Lys  Cys  Leu  Leu  His  Lys  Val  Cys  Asp  Thr  Gly  Lys
          85          90          95
Ala  Leu  Val  Ala  Val  Val  Ala  Gly  Asn  Ser  Thr  Thr  Pro  Arg  Arg  Cys
          100          105          110
Ala  Cys  Thr  Ala  Gly  Tyr  His  Trp  Ser  Gln  Asp  Cys  Glu  Cys  Cys  Arg
          115          120          125
Arg  Asn  Thr  Glu  Cys  Ala  Pro  Gly  Leu  Gly  Ala  Gln  His  Pro  Leu  Gln
          130          135          140
Leu  Asn  Lys  Asp  Thr  Val  Cys  Lys  Pro  Cys  Leu  Ala  Gly  Tyr  Phe  Ser
          145          150          155          160
Asp  Ala  Phe  Ser  Ser  Thr  Asp  Lys  Cys  Arg  Pro  Trp  Thr  Asn  Cys  Thr
          165          170          175
Phe  Leu  Gly  Lys  Arg  Val  Glu  His  His  Gly  Thr  Glu  Lys  Ser  Asp  Ala
          180          185          190
Val  Cys  Ser  Ser  Ser  Leu  Pro  Ala  Arg  Lys  Pro  Pro  Asn  Glu  Pro  His
          195          200          205
Val  Tyr  Leu  Pro  Gly  Leu  Ile  Ile  Leu  Leu  Leu  Phe  Ala  Ser  Val  Ala
          210          215          220
Leu  Val  Ala  Ala  Ile  Ile  Phe  Gly  Val  Cys  Tyr  Arg  Lys  Lys  Gly  Lys
          225          230          235          240
Ala  Leu  Thr  Ala  Asn  Leu  Trp  His  Trp  Ile  Asn  Glu  Ala  Cys  Gly  Arg
          245          250          255
Leu  Ser  Gly  Asp  Lys  Glu  Ser  Ser  Gly  Asp  Ser  Cys  Val  Ser  Thr  His
          260          265          270
Thr  Ala  Asn  Phe  Gly  Gln  Gln  Gly  Ala  Cys  Glu  Gly  Val  Leu  Leu  Leu
          275          280          285
Thr  Leu  Glu  Glu  Lys  Thr  Phe  Pro  Glu  Asp  Met  Cys  Tyr  Pro  Asp  Gln
          290          295          300
Gly  Gly  Val  Cys  Gln  Gly  Thr  Cys  Val  Gly  Gly  Gly  Pro  Tyr  Ala  Gln
          305          310          315          320
Gly  Glu  Asp  Ala  Arg  Met  Leu  Ser  Leu  Val  Ser  Lys  Thr  Glu  Ile  Glu
          325          330          335

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Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
 340 345 350
 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
 355 360 365
 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
 370 375 380
 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
 385 390 395 400
 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
 405 410 415
 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
 420 425 430
 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
 435 440 445
 Cys Arg Asn
 450

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: HOMO SAPIENS
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BONE-MARROW DERIVED DENDRITIC CELLS
 - (B) CLONE: FULL LENGTH RANK
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 39..1886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGCTGAGGC CGCGGCGCCC GCCAGCCTGT CCCGCGCC ATG GCC CCG CGC GCC	53
Met Ala Pro Arg Ala	
1 5	
CGG CGG CGC CGC CCG CTG TTC GCG CTG CTG CTG CTC TGC GCG CTG CTC	101
Arg Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu	
10 15 20	
GCC CGG CTG CAG GTG GCT TTG CAG ATC GCT CCT CCA TGT ACC AGT GAG	149
Ala Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu	
25 30 35	
AAG CAT TAT GAG CAT CTG GGA CGG TGC TGT AAC AAA TGT GAA CCA GGA	197
Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly	
40 45 50	

AAG Lys	TAC Tyr 55	ATG Met	TCT Ser	TCT Ser	AAA Lys	TGC Cys 60	ACT Thr	ACT Thr	ACC Thr	TCT Ser	GAC Asp 65	AGT Ser	GTA Val	TGT Cys	CTG Leu	245
CCC Pro 70	TGT Cys	GGC Gly	CCG Pro	GAT Asp	GAA Glu 75	TAC Tyr	TTG Leu	GAT Asp	AGC Ser	TGG Trp 80	AAT Asn	GAA Glu	GAA Glu	GAT Asp	AAA Lys 85	293
TGC Cys	TTG Leu	CTG Leu	CAT His	AAA Lys 90	GTT Val	TGT Cys	GAT Asp	ACA Thr	GGC Gly 95	AAG Lys	GCC Ala	CTG Leu	GTG Val	GCC Ala 100	GTG Val	341
GTC Val	GCC Ala	GGC Gly	AAC Asn 105	AGC Ser	ACG Thr	ACC Thr	CCC Pro	CGG Arg 110	CGC Arg	TGC Cys	GCG Ala	TGC Cys	ACG Thr 115	GCT Ala	GGG Gly	389
TAC Tyr	CAC His	TGG Trp 120	AGC Ser	CAG Gln	GAC Asp	TGC Cys	GAG Glu 125	TGC Cys	TGC Cys	CGC Arg	CGC Arg	AAC Asn 130	ACC Thr	GAG Glu	TGC Cys	437
GCG Ala 135	CCG Pro	GGC Gly	CTG Leu	GGC Gly	GCC Ala	CAG Gln 140	CAC His	CCG Pro	TTG Leu	CAG Gln	CTC Leu 145	AAC Asn	AAG Lys	GAC Asp	ACA Thr	485
GTG Val 150	TGC Cys	AAA Lys	CCT Pro	TGC Cys	CTT Leu 155	GCA Ala	GGC Gly	TAC Tyr	TTC Phe	TCT Ser 160	GAT Asp	GCC Ala	TTT Phe	TCC Ser	TCC Ser 165	533
ACG Thr	GAC Asp	AAA Lys	TGC Cys	AGA Arg 170	CCC Pro	TGG Trp	ACC Thr	AAC Asn	TGT Cys 175	ACC Thr	TTC Phe	CTT Leu	GGA Gly	AAG Lys 180	AGA Arg	581
GTA Val	GAA Glu	CAT His	CAT His 185	GGG Gly	ACA Thr	GAG Glu	AAA Lys	TCC Ser 190	GAT Asp	GCG Ala	GTT Val	TGC Cys	AGT Ser 195	TCT Ser	TCT Ser	629
CTG Leu	CCA Pro	GCT Ala 200	AGA Arg	AAA Lys	CCA Pro	CCA Pro	AAT Asn 205	GAA Glu	CCC Pro	CAT His	GTT Val 210	TAC Tyr	TTG Leu	CCC Pro	GGT Gly	677
TTA Leu 215	ATA Ile	ATT Ile	CTG Leu	CTT Leu	CTC Leu	TTC Phe 220	GCG Ala	TCT Ser	GTG Val	GCC Ala	CTG Leu 225	GTG Val	GCT Ala	GCC Ala	ATC Ile	725
ATC Ile 230	TTT Phe	GGC Gly	GTT Val	TGC Cys	TAT Tyr 235	AGG Arg	AAA Lys	AAA Lys	GGG Gly	AAA Lys 240	GCA Ala	CTC Leu	ACA Thr	GCT Ala	AAT Asn 245	773
TTG Leu	TGG Trp	CAC His	TGG Trp	ATC Ile 250	AAT Asn	GAG Glu	GCT Ala	TGT Cys	GGC Gly 255	CGC Arg	CTA Leu	AGT Ser	GGA Gly	GAT Asp 260	AAG Lys	821
GAG Glu	TCC Ser	TCA Ser	GGT Gly 265	GAC Asp	AGT Ser	TGT Cys	GTC Val	AGT Ser 270	ACA Thr	CAC His	ACG Thr	GCA Ala	AAC Asn 275	TTT Phe	GGT Gly	869
CAG Gln	CAG Gln	GGA Gly 280	GCA Ala	TGT Cys	GAA Glu	GGT Gly	GTC Val 285	TTA Leu	CTG Leu	CTG Leu	ACT Thr	CTG Leu 290	GAG Glu	GAG Glu	AAG Lys	917
ACA Thr 295	TTT Phe	CCA Pro	GAA Glu	GAT Asp	ATG Met	TGC Cys 300	TAC Tyr	CCA Pro	GAT Asp	CAA Gln	GGT Gly 305	GGT Gly	GTC Val	TGT Cys	CAG Gln	965
GGC Gly 310	ACG Thr	TGT Cys	GTA Val	GGA Gly	GGT Gly 315	GGT Gly	CCC Pro	TAC Tyr	GCA Ala	CAA Gln 320	GGC Gly	GAA Glu	GAT Asp	GCC Ala	AGG Arg 325	1013

ATG Met	CTC Leu	TCA Ser	TTG Leu	GTC Val 330	AGC Ser	AAG Lys	ACC Thr	GAG Glu	ATA Ile 335	GAG Glu	GAA Glu	GAC Asp	AGC Ser	TTC Phe 340	AGA Arg	1061
CAG Gln	ATG Met	CCC Pro	ACA Thr 345	GAA Glu	GAT Asp	GAA Glu	TAC Tyr	ATG Met 350	GAC Asp	AGG Arg	CCC Pro	TCC Ser	CAG Gln 355	CCC Pro	ACA Thr	1109
GAC Asp	CAG Gln	TTA Leu 360	CTG Leu	TTC Phe	CTC Leu	ACT Thr	GAG Glu 365	CCT Pro	GGA Gly	AGC Ser	AAA Lys	TCC Ser 370	ACA Thr	CCT Pro	CCT Pro	1157
TTC Phe	TCT Ser 375	GAA Glu	CCC Pro	CTG Leu	GAG Glu	GTG Val 380	GGG Gly	GAG Glu	AAT Asn	GAC Asp	AGT Ser 385	TTA Leu	AGC Ser	CAG Gln	TGC Cys	1205
TTC Phe 390	ACG Thr	GGG Gly	ACA Thr	CAG Gln	AGC Ser 395	ACA Thr	GTG Val	GGT Gly	TCA Ser	GAA Glu 400	AGC Ser	TGC Cys	AAC Asn	TGC Cys	ACT Thr 405	1253
GAG Glu	CCC Pro	CTG Leu	TGC Cys	AGG Arg 410	ACT Thr	GAT Asp	TGG Trp	ACT Thr	CCC Pro 415	ATG Met	TCC Ser	TCT Ser	GAA Glu	AAC Asn 420	TAC Tyr	1301
TTG Leu	CAA Gln	AAA Lys	GAG Glu 425	GTG Val	GAC Asp	AGT Ser	GGC Gly	CAT His 430	TGC Cys	CCG Pro	CAC His	TGG Trp	GCA Ala 435	GCC Ala	AGC Ser	1349
CCC Pro	AGC Ser	CCC Pro 440	AAC Asn	TGG Trp	GCA Ala	GAT Asp	GTC Val 445	TGC Cys	ACA Thr	GGC Gly	TGC Cys	CGG Arg 450	AAC Asn	CCT Pro	CCT Pro	1397
GGG Gly 455	GAG Glu	GAC Asp	TGT Cys	GAA Glu	CCC Pro	CTC Leu 460	GTG Val	GGT Gly	TCC Ser	CCA Pro	AAA Lys 465	CGT Arg	GGA Gly	CCC Pro	TTG Leu	1445
CCC Pro 470	CAG Gln	TGC Cys	GCC Ala	TAT Tyr 475	GGC Gly	ATG Met	GGC Gly	CTT Leu	CCC Pro 480	CCT Pro	GAA Glu	GAA Glu	GAA Glu	GCC Ala	AGC Ser 485	1493
AGG Arg	ACG Thr	GAG Glu	GCC Ala 490	AGA Arg	GAC Asp	CAG Gln	CCC Pro	GAG Glu 495	GAT Asp	GGG Gly	GCT Ala	GAT Asp	GGG Gly 500	AGG Arg	CTC Leu	1541
CCA Pro	AGC Ser	TCA Ser	GCG Ala 505	AGG Arg	GCA Ala	GGT Gly	GCC Ala 510	GGG Gly	TCT Ser	GGA Gly	AGC Ser	TCC Ser	CCT Pro 515	GGT Gly	GGC Gly	1589
CAG Gln	TCC Ser	CCT Pro 520	GCA Ala	TCT Ser	GGA Gly	AAT Asn	GTG Val 525	ACT Thr	GGA Gly	AAC Asn	AGT Ser 530	AAC Asn	TCC Ser	ACG Thr	TTC Phe	1637
ATC Ile 535	TCC Ser	AGC Ser	GGG Gly	CAG Gln	GTG Val	ATG Met 540	AAC Asn	TTC Phe	AAG Lys	GGC Gly	GAC Asp 545	ATC Ile	ATC Ile	GTG Val	GTC Val	1685
TAC Tyr 550	GTC Val	AGC Ser	CAG Gln	ACC Thr	TCG Ser 555	CAG Gln	GAG Glu	GGC Gly	GCG Ala	GCG Ala 560	GCG Ala	GCT Ala	GCG Ala	GAG Glu	CCC Pro 565	1733
ATG Met	GGC Gly	CGC Arg	CCG Pro	GTG Val 570	CAG Gln	GAG Glu	GAG Glu	ACC Thr	CTG Leu 575	GCG Ala	CGC Arg	CGA Arg	GAC Asp	TCC Ser 580	TTC Phe	1781
GCG Ala	GGG Gly	AAC Asn	GGC Gly 585	CCG Pro	CGC Arg	TTC Phe	CCG Pro	GAC Asp 590	CCG Pro	TGC Cys	GGC Gly	GGC Gly	CCC Pro 595	GAG Glu	GGG Gly	1829

CTG CGG GAG CCG GAG AAG GCC TCG AGG CCG GTG CAG GAG CAA GGC GGG	1877
Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly	
600 605 610	
GCC AAG GCT TGAGCGCCCC CCATGGCTGG GAGCCCCGAAG CTCGGAGCCA	1926
Ala Lys Ala	
615	
GGGCTCGCGA GGGCAGCACC GCAGCCTCTG CCCCAGCCCC GGCCACCCAG GGATCGATCG	1986
GTACAGTCGA GGAAGACCAC CCGGCATTCT CTGCCCACTT TGCCTTCCAG GAAATGGGCT	2046
TTTCAGGAAG TGAATTGATG AGGACTGTCC CCATGCCAC GGTATGCTCAG CAGCCCCGCCG	2106
CACTGGGGCA GATGTCTCCC CTGCCACTCC TCAAACTCGC AGCAGTAATT TGTGGCACTA	2166
TGACAGCTAT TTTTATGACT ATCCTGTTCT GTGGGGGGGG GGTCTATGTT TTCCCCCAT	2226
ATTTGTATTC CTTTTCATAA CTTTCTTGA TATCTTTCCT CCCTCTTTTT TAATGTAAAG	2286
GTTTTCTCAA AAATTCTCCT AAAGGTGAGG GTCTCTTCT TTTCTTTTTT CCTTTTTTTT	2346
TTCTTTTTTT GGCAACCTGG CTCTGGCCCA GGCTAGAGTG CAGTGGTGCG ATTATAGCCC	2406
GGTGCAGCCT CTAACCTCTG GGCTCAAGCA ATCCAAGTGA TCCTCCCACC TCAACCTTCG	2466
GAGTAGCTGG GATCACAGCT GCAGGCCACG CCCAGCTTCC TCCCCCGAC TCCCCCCCCC	2526
CAGAGACACG GTCCCACCAT GTTACCCAGC CTGGTCTCAA ACTCCCCAGC TAAAGCAGTC	2586
CTCCAGCCTC GGCTTCCAA AGTACTGGGA TTACAGGCGT GAGCCCCAC GCTGGCCTGC	2646
TTTACGTATT TTCTTTTGTG CCCCTGCTCA CAGTGTTTTA GAGATGGCTT TCCCAGTGTG	2706
TGTTCAATTGT AAACACTTTT GGGAAAGGGC TAAACATGTG AGGCCTGGAG ATAGTTGCTA	2766
AGTTGCTAGG AACATGTGGT GGGACTTTCA TATTCTGAAA AATGTTCTAT ATTCTCATTT	2826
TTCTAAAAGA AAGAAAAAAG GAAACCCGAT TTATTTCTCC TGAATCTTTT TAAGTTTGTG	2886
TCGTTCTTA AGCAGAACTA AGCTCAGTAT GTGACCTTAC CCGCTAGGTG GTTAATTTAT	2946
CCATGCTGGC AGAGGCACTC AGGTACTTGG TAAGCAAATT TCTAAACTC CAAGTTGCTG	3006
CAGCTTGGCA TTCTTCTTAT TCTAGAGGTC TCTCTGAAA AGATGGAGAA AATGAACAGG	3066
ACATGGGGCT CCTGGAAAGA AAGGGCCCGG GAAGTTCAAG GAAGAATAAA GTTGAAATTT	3126
TAAAAAAA	3136

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Pro	Leu	Phe	Ala	Leu	Leu	Leu
1				5					10					15	
Leu	Cys	Ala	Leu	Leu	Ala	Arg	Leu	Gln	Val	Ala	Leu	Gln	Ile	Ala	Pro
			20					25					30		
Pro	Cys	Thr	Ser	Glu	Lys	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	Asn
		35					40					45			

Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
 50 55 60
 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
 65 70 75 80
 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
 85 90 95
 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
 100 105 110
 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
 115 120 125
 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
 130 135 140
 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
 145 150 155 160
 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
 165 170 175
 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
 180 185 190
 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
 195 200 205
 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
 210 215 220
 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
 225 230 235 240
 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
 245 250 255
 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
 260 265 270
 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
 275 280 285
 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
 290 295 300
 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
 305 310 315 320
 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
 325 330 335
 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
 340 345 350
 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
 355 360 365
 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
 370 375 380
 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
 385 390 395 400
 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
 405 410 415

Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
 420 425 430
 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
 435 440 445
 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
 450 455 460
 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
 465 470 475 480
 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
 485 490 495
 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly
 500 505 510
 Ser Ser Pro Gly Gly Gln Ser Pro Ala Ser Gly Asn Val Thr Gly Asn
 515 520 525
 Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met Asn Phe Lys Gly
 530 535 540
 Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln Glu Gly Ala Ala
 545 550 555 560
 Ala Ala Ala Glu Pro Met Gly Arg Pro Val Gln Glu Glu Thr Leu Ala
 565 570 575
 Arg Arg Asp Ser Phe Ala Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys
 580 585 590
 Gly Gly Pro Glu Gly Leu Arg Glu Pro Glu Lys Ala Ser Arg Pro Val
 595 600 605
 Gln Glu Gln Gly Gly Ala Lys Ala
 610 615

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: FLAG® peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc mutein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15
 Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 65 70 75 80
 Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 85 90 95
 Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
 100 105 110
 Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 115 120 125
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
 145 150 155 160
 His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220
 Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: CMV (R2780 Leader)

(ix) FEATURE:

(D) OTHER INFORMATION: Met1-Arg28 is the actual leader peptide; Arg29 strengthens the furin cleavage site; nucleotides encoding Thr30 and Ser31 add a SpeI site.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr
1           5           10           15

Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser
          20           25           30

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1630 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:
 (B) CLONE: RANKL

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 3..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CC GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG      47
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro
1           5           10           15

GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC      95
Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu
          20           25           30

CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG     143
Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu
          35           40           45

TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT     191
Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr
          50           55           60

CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GAT TTG CAG     239
His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln
          65           70           75

GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG     287
Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg
          80           85           90           95

ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT     335
Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile
          100           105           110

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GTG	GGG	CCA	CAG	CGC	TTC	TCA	GGA	GCT	CCA	GCT	ATG	ATG	GAA	GGC	TCA	383
Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala	Met	Met	Glu	Gly	Ser	
			115					120					125			
TGG	TTG	GAT	GTG	GCC	CAG	CGA	GGC	AAG	CCT	GAG	GCC	CAG	CCA	TTT	GCA	431
Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu	Ala	Gln	Pro	Phe	Ala	
		130					135					140				
CAC	CTC	ACC	ATC	AAT	GCT	GCC	AGC	ATC	CCA	TCG	GGT	TCC	CAT	AAA	GTC	479
His	Leu	Thr	Ile	Asn	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val		
	145				150					155						
ACT	CTG	TCC	TCT	TGG	TAC	CAC	GAT	CGA	GGC	TGG	GCC	AAG	ATC	TCT	AAC	527
Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Asn	
160					165					170					175	
ATG	ACG	TTA	AGC	AAC	GGA	AAA	CTA	AGG	GTT	AAC	CAA	GAT	GGC	TTC	TAT	575
Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn	Gln	Asp	Gly	Phe	Tyr	
				180					185					190		
TAC	CTG	TAC	GCC	AAC	ATT	TGC	TTT	CGG	CAT	CAT	GAA	ACA	TCG	GGA	AGC	623
Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His	Glu	Thr	Ser	Gly	Ser	
			195					200					205			
GTA	CCT	ACA	GAC	TAT	CTT	CAG	CTG	ATG	GTG	TAT	GTC	GTT	AAA	ACC	AGC	671
Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr	Val	Val	Lys	Thr	Ser	
		210					215					220				
ATC	AAA	ATC	CCA	AGT	TCT	CAT	AAC	CTG	ATG	AAA	GGA	GGG	AGC	ACG	AAA	719
Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys	Gly	Gly	Ser	Thr	Lys	
	225					230					235					
AAC	TGG	TCG	GGC	AAT	TCT	GAA	TTC	CAC	TTT	TAT	TCC	ATA	AAT	GTT	GGG	767
Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr	Ser	Ile	Asn	Val	Gly	
240					245					250					255	
GGA	TTT	TTC	AAG	CTC	CGA	GCT	GGT	GAA	GAA	ATT	AGC	ATT	CAG	GTG	TCC	815
Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile	Ser	Ile	Gln	Val	Ser	
				260				265						270		
AAC	CCT	TCC	CTG	CTG	GAT	CCG	GAT	CAA	GAT	GCG	ACG	TAC	TTT	GGG	GCT	863
Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	
			275					280					285			
TTC	AAA	GTT	CAG	GAC	ATA	GAC	TGAGACTCAT	TTCGTGGAAC	ATTAGCATGG							914
Phe	Lys	Val	Gln	Asp	Ile	Asp										
		290														
ATGTCCTAGA	TGTTTTGGAAA	CTTCTTAAAA	AATGGATGAT	GTCTATACAT	GTGTAAGACT											974
ACTAAGAGAC	ATGGCCACG	GTGTATGAAA	CTCACAGCCC	TCTCTCTTGA	GCCTGTACAG											1034
GTTGTGTATA	TGTAAAGTCC	ATAGGTGATG	TTAGATTTCAT	GGTGATTACA	CAACGGTTTT											1094
ACAATTTTGT	AATGATTTC	TAGAATTGAA	CCAGATTGGG	AGAGGTATTC	CGATGCTTAT											1154
GAAAACTTA	CACGTGAGCT	ATGGAAGGGG	GTCACAGTCT	CTGGGTCTAA	CCCCTGGACA											1214
TGTGCCACTG	AGAACCTTGA	AATTAAGAGG	ATGCCATGTC	ATTGCAAAGA	AATGATAGTG											1274
TGAAGGGTTA	AGTTCTTTTG	AATTGTTACA	TTGCGCTGGG	ACCTGCAAAT	AAGTTCTTTT											1334
TTTCTAATGA	GGAGAGAAAA	ATATATGTAT	TTTTATATAA	TGTCTAAAGT	TATATTTTCA											1394
GTGTAATGTT	TTCTGTGCAA	AGTTTTGTAA	ATTATATTTG	TGCTATAGTA	TTTGATTCAA											1454
AATATTTAAA	AATGTCTCAC	TGTTGACATA	TTTAATGTTT	TAAATGTACA	GATGTATTTA											1514
ACTGGTGCAC	TTTGTAATTC	CCCTGAAGGT	ACTCGTAGCT	AAGGGGGCAG	AATACTGTTT											1574

CTGGTGACCA CATGTAGTTT ATTTCTTTAT TCTTTTAAAC TTAATAGAGT CTTCAG

1630

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
 1 5 10 15
 Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
 20 25 30
 Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
 35 40 45
 Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
 50 55 60
 Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Asp Leu Gln Asp
 65 70 75 80
 Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
 85 90 95
 Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
 100 105 110
 Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
 115 120 125
 Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
 130 135 140
 Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
 145 150 155 160
 Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
 165 170 175
 Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
 180 185 190
 Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
 195 200 205
 Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
 210 215 220
 Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
 225 230 235 240
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 245 250 255
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 260 265 270
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 275 280 285
 Lys Val Gln Asp Ile Asp
 290

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 (A) LIBRARY:
 (B) CLONE: huRANKL (full length)
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..951
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	CGC	CGC	GCC	AGC	AGA	GAC	TAC	ACC	AAG	TAC	CTG	CGT	GGC	TCG	GAG	48
Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	
1				5					10					15		
GAG	ATG	GGC	GGC	GGC	CCC	GGA	GCC	CCG	CAC	GAG	GGC	CCC	CTG	CAC	GCC	96
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala	
		20						25					30			
CCG	CCG	CCG	CCT	GCG	CCG	CAC	CAG	CCC	CCC	GCC	GCC	TCC	CGC	TCC	ATG	144
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	
		35					40					45				
TTC	GTG	GCC	CTC	CTG	GGG	CTG	GGG	CTG	GGC	CAG	GTT	GTC	TGC	AGC	GTC	192
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	
	50				55						60					
GCC	CTG	TTC	TTC	TAT	TTC	AGA	GCG	CAG	ATG	GAT	CCT	AAT	AGA	ATA	TCA	240
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	
65					70				75						80	
GAA	GAT	GGC	ACT	CAC	TGC	ATT	TAT	AGA	ATT	TTG	AGA	CTC	CAT	GAA	AAT	288
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	
			85						90					95		
GCA	GAT	TTT	CAA	GAC	ACA	ACT	CTG	GAG	AGT	CAA	GAT	ACA	AAA	TTA	ATA	336
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	
		100						105					110			
CCT	GAT	TCA	TGT	AGG	AGA	ATT	AAA	CAG	GCC	TTT	CAA	GGA	GCT	GTG	CAA	384
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	
		115					120					125				
AAG	GAA	TTA	CAA	CAT	ATC	GTT	GGA	TCA	CAG	CAC	ATC	AGA	GCA	GAG	AAA	432
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	
	130				135						140					
GCG	ATG	GTG	GAT	GGC	TCA	TGG	TTA	GAT	CTG	GCC	AAG	AGG	AGC	AAG	CTT	480
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	
145					150					155					160	

GAA	GCT	CAG	CCT	TTT	GCT	CAT	CTC	ACT	ATT	AAT	GCC	ACC	GAC	ATC	CCA	528
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Thr	Asp	Ile	Pro	
				165					170					175		
TCT	GGT	TCC	CAT	AAA	GTG	AGT	CTG	TCC	TCT	TGG	TAC	CAT	GAT	CGG	GGT	576
Ser	Gly	Ser	His	Lys	Val	Ser	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
			180					185					190			
TGG	GCC	AAG	ATC	TCC	AAC	ATG	ACT	TTT	AGC	AAT	GGA	AAA	CTA	ATA	GTT	624
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Phe	Ser	Asn	Gly	Lys	Leu	Ile	Val	
		195					200				205					
AAT	CAG	GAT	GGC	TTT	TAT	TAC	CTG	TAT	GCC	AAC	ATT	TGC	TTT	CGA	CAT	672
Asn	Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	
	210					215					220					
CAT	GAA	ACT	TCA	GGA	GAC	CTA	GCT	ACA	GAG	TAT	CTT	CAA	CTA	ATG	GTG	720
His	Glu	Thr	Ser	Gly	Asp	Leu	Ala	Thr	Glu	Tyr	Leu	Gln	Leu	Met	Val	
	225				230					235					240	
TAC	GTC	ACT	AAA	ACC	AGC	ATC	AAA	ATC	CCA	AGT	TCT	CAT	ACC	CTG	ATG	768
Tyr	Val	Thr	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Thr	Leu	Met	
				245					250					255		
AAA	GGA	GGA	AGC	ACC	AAG	TAT	TGG	TCA	GGG	AAT	TCT	GAA	TTC	CAT	TTT	816
Lys	Gly	Gly	Ser	Thr	Lys	Tyr	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
			260					265					270			
TAT	TCC	ATA	AAC	GTT	GGT	GGA	TTT	TTT	AAG	TTA	CGG	TCT	GGA	GAG	GAA	864
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ser	Gly	Glu	Glu	
		275					280					285				
ATC	AGC	ATC	GAG	GTC	TCC	AAC	CCC	TCC	TTA	CTG	GAT	CCG	GAT	CAG	GAT	912
Ile	Ser	Ile	Glu	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
	290					295					300					
GCA	ACA	TAC	TTT	GGG	GCT	TTT	AAA	GTT	CGA	GAT	ATA	GAT	TGA			954
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Arg	Asp	Ile	Asp				
					310					315						

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	
1				5					10					15		
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala	
			20					25					30			
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	
		35					40					45				
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	
	50					55					60					
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	
	65				70					75					80	
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	
				85					90					95		

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110
 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125
 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140
 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 260 265 270
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 275 280 285
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 290 295 300
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1878 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Murine
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Murine Fetal Liver Epithelium
 - (B) CLONE: muRANK
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG	GCC	CCG	CGC	GCC	CGG	CGG	CGC	CGC	CAG	CTG	CCC	GCG	CCG	CTG	CTG	48
Met	Ala	Pro	Arg	Ala	Arg	Arg	Arg	Arg	Gln	Leu	Pro	Ala	Pro	Leu	Leu	
1				5					10					15		
GCG	CTC	TGC	GTG	CTG	CTC	GTT	CCA	CTG	CAG	GTG	ACT	CTC	CAG	GTC	ACT	96
Ala	Leu	Cys	Val	Leu	Leu	Val	Pro	Leu	Gln	Val	Thr	Leu	Gln	Val	Thr	
			20					25					30			
CCT	CCA	TGC	ACC	CAG	GAG	AGG	CAT	TAT	GAG	CAT	CTC	GGA	CGG	TGT	TGC	144
Pro	Pro	Cys	Thr	Gln	Glu	Arg	His	Tyr	Glu	His	Leu	Gly	Arg	Cys	Cys	
		35					40					45				
AGC	AGA	TGC	GAA	CCA	GGA	AAG	TAC	CTG	TCC	TCT	AAG	TGC	ACT	CCT	ACC	192
Ser	Arg	Cys	Glu	Pro	Gly	Lys	Tyr	Leu	Ser	Ser	Lys	Cys	Thr	Pro	Thr	
	50					55					60					
TCC	GAC	AGT	GTG	TGT	CTG	CCC	TGT	GGC	CCC	GAT	GAG	TAC	TTG	GAC	ACC	240
Ser	Asp	Ser	Val	Cys	Leu	Pro	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Thr	
65					70					75					80	
TGG	AAT	GAA	GAA	GAT	AAA	TGC	TTG	CTG	CAT	AAA	GTC	TGT	GAT	GCA	GGC	288
Trp	Asn	Glu	Glu	Asp	Lys	Cys	Leu	Leu	His	Lys	Val	Cys	Asp	Ala	Gly	
				85					90					95		
AAG	GCC	CTG	GTG	GCG	GTG	GAT	CCT	GGC	AAC	CAC	ACG	GCC	CCG	CGT	CGC	336
Lys	Ala	Leu	Val	Ala	Val	Asp	Pro	Gly	Asn	His	Thr	Ala	Pro	Arg	Arg	
			100					105					110			
TGT	GCT	TGC	ACG	GCT	GGC	TAC	CAC	TGG	AAC	TCA	GAC	TGC	GAG	TGC	TGC	384
Cys	Ala	Cys	Thr	Ala	Gly	Tyr	His	Trp	Asn	Ser	Asp	Cys	Glu	Cys	Cys	
		115					120					125				
CGC	AGG	AAC	ACG	GAG	TGT	GCA	CCT	GGC	TTC	GGA	GCT	CAG	CAT	CCC	TTG	432
Arg	Arg	Asn	Thr	Glu	Cys	Ala	Pro	Gly	Phe	Gly	Ala	Gln	His	Pro	Leu	
	130					135					140					
CAG	CTC	AAC	AAG	GAT	ACG	GTG	TGC	ACA	CCC	TGC	CTC	CTG	GGC	TTC	TTC	480
Gln	Leu	Asn	Lys	Asp	Thr	Val	Cys	Thr	Pro	Cys	Leu	Leu	Gly	Phe	Phe	
145					150					155					160	
TCA	GAT	GTC	TTT	TCG	TCC	ACA	GAC	AAA	TGC	AAA	CCT	TGG	ACC	AAC	TGC	528
Ser	Asp	Val	Phe	Ser	Ser	Thr	Asp	Lys	Cys	Lys	Pro	Trp	Thr	Asn	Cys	
				165					170					175		
ACC	CTC	CTT	GGA	AAG	CTA	GAA	GCA	CAC	CAG	GGG	ACA	ACG	GAA	TCA	GAT	576
Thr	Leu	Leu	Gly	Lys	Leu	Glu	Ala	His	Gln	Gly	Thr	Thr	Glu	Ser	Asp	
			180					185					190			
GTG	GTC	TGC	AGC	TCT	TCC	ATG	ACA	CTG	AGG	AGA	CCA	CCC	AAG	GAG	GCC	624
Val	Val	Cys	Ser	Ser	Ser	Met	Thr	Leu	Arg	Arg	Pro	Pro	Lys	Glu	Ala	
		195					200					205				
CAG	GCT	TAC	CTG	CCC	AGT	CTC	ATC	GTT	CTG	CTC	CTC	TTC	ATC	TCT	GTG	672
Gln	Ala	Tyr	Leu	Pro	Ser	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ile	Ser	Val	
	210					215					220					
GTA	GTA	GTG	GCT	GCC	ATC	ATC	TTC	GGC	GTT	TAC	TAC	AGG	AAG	GGA	GGG	720
Val	Val	Val	Ala	Ala	Ile	Ile	Phe	Gly	Val	Tyr	Tyr	Arg	Lys	Gly	Gly	
225					230				235					240		
AAA	GCG	CTG	ACA	GCT	AAT	TTG	TGG	AAT	TGG	GTC	AAT	GAT	GCT	TGC	AGT	768
Lys	Ala	Leu	Thr	Ala	Asn	Leu	Trp	Asn	Trp	Val	Asn	Asp	Ala	Cys	Ser	
				245					250					255		
AGT	CTA	AGT	GGA	AAT	AAG	GAG	TCC	TCA	GGG	GAC	CGT	TGT	GCT	GGT	TCC	816
Ser	Leu	Ser	Gly	Asn	Lys	Glu	Ser	Ser	Gly	Asp	Arg	Cys	Ala	Gly	Ser	
			260					265					270			

CAC	TCG	GCA	ACC	TCC	AGT	CAG	CAA	GAA	GTG	TGT	GAA	GGT	ATC	TTA	CTA	864
His	Ser	Ala	Thr	Ser	Ser	Gln	Gln	Glu	Val	Cys	Glu	Gly	Ile	Leu	Leu	
		275					280					285				
ATG	ACT	CGG	GAG	GAG	AAG	ATG	GTT	CCA	GAA	GAC	GGT	GCT	GGA	GTC	TGT	912
Met	Thr	Arg	Glu	Glu	Lys	Met	Val	Pro	Glu	Asp	Gly	Ala	Gly	Val	Cys	
	290					295					300					
GGG	CCT	GTG	TGT	GCG	GCA	GGT	GGG	CCC	TGG	GCA	GAA	GTC	AGA	GAT	TCT	960
Gly	Pro	Val	Cys	Ala	Ala	Gly	Gly	Pro	Trp	Ala	Glu	Val	Arg	Asp	Ser	
305					310					315					320	
AGG	ACG	TTC	ACA	CTG	GTC	AGC	GAG	GTT	GAG	ACG	CAA	GGA	GAC	CTC	TCG	1008
Arg	Thr	Phe	Thr	Leu	Val	Ser	Glu	Val	Glu	Thr	Gln	Gly	Asp	Leu	Ser	
				325					330					335		
AGG	AAG	ATT	CCC	ACA	GAG	GAT	GAG	TAC	ACG	GAC	CGG	CCC	TCG	CAG	CCT	1056
Arg	Lys	Ile	Pro	Thr	Glu	Asp	Glu	Tyr	Thr	Asp	Arg	Pro	Pro	Gln	Pro	
			340					345					350			
TCG	ACT	GGT	TCA	CTG	CTC	CTA	ATC	CAG	CAG	GGA	AGC	AAA	TCT	ATA	CCC	1104
Ser	Thr	Gly	Ser	Leu	Leu	Leu	Ile	Gln	Gln	Gly	Ser	Lys	Ser	Ile	Pro	
		355					360					365				
CCA	TTC	CAG	GAG	CCC	CTG	GAA	GTG	GGG	GAG	AAC	GAC	AGT	TTA	AGC	CAG	1152
Pro	Phe	Gln	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	
	370					375					380					
TGT	TTC	ACC	GGG	ACT	GAA	AGC	ACG	GTG	GAT	TCT	GAG	GGC	TGT	GAC	TTC	1200
Cys	Phe	Thr	Gly	Thr	Glu	Ser	Thr	Val	Asp	Ser	Glu	Gly	Cys	Asp	Phe	
385					390					395					400	
ACT	GAG	CCT	CCG	AGC	AGA	ACT	GAC	TCT	ATG	CCC	GTG	TCC	CCT	GAA	AAG	1248
Thr	Glu	Pro	Pro	Ser	Arg	Thr	Asp	Ser	Met	Pro	Val	Ser	Pro	Glu	Lys	
				405					410					415		
CAC	CTG	ACA	AAA	GAA	ATA	GAA	GGT	GAC	AGT	TGC	CTC	CCC	TGG	GTG	GTC	1296
His	Leu	Thr	Lys	Glu	Ile	Glu	Gly	Asp	Ser	Cys	Leu	Pro	Trp	Val	Val	
			420					425					430			
AGC	TCC	AAC	TCA	ACA	GAT	GGC	TAC	ACA	GGC	AGT	GGG	AAC	ACT	CCT	GGG	1344
Ser	Ser	Asn	Ser	Thr	Asp	Gly	Tyr	Thr	Gly	Ser	Gly	Asn	Thr	Pro	Gly	
		435					440					445				
GAG	GAC	CAT	GAA	CCC	TTT	CCA	GGG	TCC	CTG	AAA	TGT	GGA	CCA	TTG	CCC	1392
Glu	Asp	His	Glu	Pro	Phe	Pro	Gly	Ser	Leu	Lys	Cys	Gly	Pro	Leu	Pro	
	450					455					460					
CAG	TGT	GCC	TAC	AGC	ATG	GGC	TTT	CCC	AGT	GAA	GCA	GCA	GCC	AGC	ATG	1440
Gln	Cys	Ala	Tyr	Ser	Met	Gly	Phe	Pro	Ser	Glu	Ala	Ala	Ala	Ser	Met	
465					470					475					480	
GCA	GAG	GCG	GGA	GTA	CGG	CCC	CAG	GAC	AGG	GCT	GAT	GAG	AGG	GGA	GCC	1488
Ala	Glu	Ala	Gly	Val	Arg	Pro	Gln	Asp	Arg	Ala	Asp	Glu	Arg	Gly	Ala	
				485					490					495		
TCA	GGG	TCC	GGG	AGC	TCC	CCC	AGT	GAC	CAG	CCA	CCT	GCC	TCT	GGG	AAC	1536
Ser	Gly	Ser	Gly	Ser	Ser	Pro	Ser	Asp	Gln	Pro	Pro	Ala	Ser	Gly	Asn	
			500					505					510			
GTG	ACT	GGA	AAC	AGT	AAC	TCC	ACG	TTC	ATC	TCT	AGC	GGG	CAG	GTG	ATG	1584
Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	Ser	Ser	Gly	Gln	Val	Met	
		515					520					525				
AAC	TTC	AAG	GGT	GAC	ATC	ATC	GTG	GTG	TAT	GTC	AGC	CAG	ACC	TCG	CAG	1632
Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	Val	Ser	Gln	Thr	Ser	Gln	
	530					535					540					
GAG	GGC	CCG	GGT	TCC	GCA	GAG	CCC	GAG	TCG	GAG	CCC	GTG	GGC	CGC	CCT	1680

Glu 545	Gly	Pro	Gly	Ser	Ala 550	Glu	Pro	Glu	Ser	Glu 555	Pro	Val	Gly	Arg	Pro 560		
GTG	CAG	GAG	GAG	ACG	CTG	GCA	CAC	AGA	GAC	TCC	TTT	GCG	GGC	ACC	GCG	1728	
Val	Gln	Glu	Glu	Thr 565	Leu	Ala	His	Arg	Asp 570	Ser	Phe	Ala	Gly	Thr 575	Ala		
CCG	CGC	TTC	CCC	GAC	GTC	TGT	GCC	ACC	GGG	GCT	GGG	CTG	CAG	GAG	CAG	1776	
Pro	Arg	Phe	Pro 580	Asp	Val	Cys	Ala	Thr 585	Gly	Ala	Gly	Leu	Gln 590	Glu	Gln		
GGG	GCA	CCC	CGG	CAG	AAG	GAC	GGG	ACA	TCG	CGG	CCG	GTG	CAG	GAG	CAG	1824	
Gly	Ala	Pro 595	Arg	Gln	Lys	Asp	Gly 600	Thr	Ser	Arg	Pro	Val 605	Gln	Glu	Gln		
GGT	GGG	GCG	CAG	ACT	TCA	CTC	CAT	ACC	CAG	GGG	TCC	GGA	CAA	TGT	GCA	1872	
Gly	Gly	Ala	Gln	Thr	Ser	Leu	His	Thr	Gln	Gly	Ser	Gly	Gln	Cys	Ala		
610						615				620							
GAA	TGA															1878	
Glu 625																	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met 1	Ala	Pro	Arg	Ala 5	Arg	Arg	Arg	Arg	Gln 10	Leu	Pro	Ala	Pro	Leu 15	Leu		
Ala	Leu	Cys	Val 20	Leu	Leu	Val	Pro	Leu 25	Gln	Val	Thr	Leu	Gln 30	Val	Thr		
Pro	Pro	Cys 35	Thr	Gln	Glu	Arg	His 40	Tyr	Glu	His	Leu	Gly 45	Arg	Cys	Cys		
Ser 50	Arg	Cys	Glu	Pro	Gly	Lys 55	Tyr	Leu	Ser	Ser	Lys 60	Cys	Thr	Pro	Thr		
Ser 65	Asp	Ser	Val	Cys	Leu 70	Pro	Cys	Gly	Pro	Asp 75	Glu	Tyr	Leu	Asp	Thr 80		
Trp	Asn	Glu	Glu 85	Asp	Lys	Cys	Leu	Leu	His 90	Lys	Val	Cys	Asp	Ala 95	Gly		
Lys	Ala	Leu	Val 100	Ala	Val	Asp	Pro	Gly 105	Asn	His	Thr	Ala	Pro 110	Arg	Arg		
Cys	Ala	Cys 115	Thr	Ala	Gly	Tyr	His 120	Trp	Asn	Ser	Asp	Cys 125	Glu	Cys	Cys		
Arg 130	Arg	Asn	Thr	Glu	Cys	Ala 135	Pro	Gly	Phe	Gly	Ala 140	Gln	His	Pro	Leu		
Gln 145	Leu	Asn	Lys	Asp	Thr 150	Val	Cys	Thr	Pro	Cys 155	Leu	Leu	Gly	Phe	Phe 160		
Ser	Asp	Val	Phe	Ser 165	Ser	Thr	Asp	Lys	Cys 170	Lys	Pro	Trp	Thr	Asn 175	Cys		
Thr	Leu	Leu	Gly 180	Lys	Leu	Glu	Ala	His 185	Gln	Gly	Thr	Thr	Glu 190	Ser	Asp		

Val Val Cys Ser Ser Ser Met Thr Leu Arg Arg Pro Pro Lys Glu Ala
 195 200 205
 Gln Ala Tyr Leu Pro Ser Leu Ile Val Leu Leu Leu Phe Ile Ser Val
 210 215 220
 Val Val Val Ala Ala Ile Ile Phe Gly Val Tyr Tyr Arg Lys Gly Gly
 225 230 235 240
 Lys Ala Leu Thr Ala Asn Leu Trp Asn Trp Val Asn Asp Ala Cys Ser
 245 250 255
 Ser Leu Ser Gly Asn Lys Glu Ser Ser Gly Asp Arg Cys Ala Gly Ser
 260 265 270
 His Ser Ala Thr Ser Ser Gln Gln Glu Val Cys Glu Gly Ile Leu Leu
 275 280 285
 Met Thr Arg Glu Glu Lys Met Val Pro Glu Asp Gly Ala Gly Val Cys
 290 295 300
 Gly Pro Val Cys Ala Ala Gly Gly Pro Trp Ala Glu Val Arg Asp Ser
 305 310 315 320
 Arg Thr Phe Thr Leu Val Ser Glu Val Glu Thr Gln Gly Asp Leu Ser
 325 330 335
 Arg Lys Ile Pro Thr Glu Asp Glu Tyr Thr Asp Arg Pro Ser Gln Pro
 340 345 350
 Ser Thr Gly Ser Leu Leu Leu Ile Gln Gln Gly Ser Lys Ser Ile Pro
 355 360 365
 Pro Phe Gln Glu Pro Leu Glu Val Gly Glu Asn Asp Ser Leu Ser Gln
 370 375 380
 Cys Phe Thr Gly Thr Glu Ser Thr Val Asp Ser Glu Gly Cys Asp Phe
 385 390 395 400
 Thr Glu Pro Pro Ser Arg Thr Asp Ser Met Pro Val Ser Pro Glu Lys
 405 410 415
 His Leu Thr Lys Glu Ile Glu Gly Asp Ser Cys Leu Pro Trp Val Val
 420 425 430
 Ser Ser Asn Ser Thr Asp Gly Tyr Thr Gly Ser Gly Asn Thr Pro Gly
 435 440 445
 Glu Asp His Glu Pro Phe Pro Gly Ser Leu Lys Cys Gly Pro Leu Pro
 450 455 460
 Gln Cys Ala Tyr Ser Met Gly Phe Pro Ser Glu Ala Ala Ala Ser Met
 465 470 475 480
 Ala Glu Ala Gly Val Arg Pro Gln Asp Arg Ala Asp Glu Arg Gly Ala
 485 490 495
 Ser Gly Ser Gly Ser Ser Pro Ser Asp Gln Pro Pro Ala Ser Gly Asn
 500 505 510
 Val Thr Gly Asn Ser Asn Ser Thr Phe Ile Ser Ser Gly Gln Val Met
 515 520 525
 Asn Phe Lys Gly Asp Ile Ile Val Val Tyr Val Ser Gln Thr Ser Gln
 530 535 540
 Glu Gly Pro Gly Ser Ala Glu Pro Glu Ser Glu Pro Val Gly Arg Pro
 545 550 555 560

Val Gln Glu Glu Thr Leu Ala His Arg Asp Ser Phe Ala Gly Thr Ala
565 570 575
Pro Arg Phe Pro Asp Val Cys Ala Thr Gly Ala Gly Leu Gln Glu Gln
580 585 590
Gly Ala Pro Arg Gln Lys Asp Gly Thr Ser Arg Pro Val Gln Glu Gln
595 600 605
Gly Gly Ala Gln Thr Ser Leu His Thr Gln Gly Ser Gly Gln Cys Ala
610 615 620
Glu
625

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Tyr Lys Asp Glu
5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His His His His His His
5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
20 25 30

Arg